



st0005seq
SEQUENCE LISTING

<110> AVENTIS PHARMACEUTICALS, INC.

<120> COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF PARKIN

<130> ST00005

<140>

<141>

<160> 46

<170> PatentIn Ver. 2.1

<210> 1

<211> 1313

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1032)

<400> 1

cag	aat	ctc	cca	tcc	agt	ccg	gca	ccc	agt	acc	ata	ttc	tct	gga	ggt	48
Gln	Asn	Leu	Pro	Ser	Ser	Pro	Ala	Pro	Ser	Thr	Ile	Phe	Ser	Gly	Gly	
1				5					10					15		
ttt	aga	cac	gga	agt	tta	att	agc	att	gac	agc	acc	tgt	aca	gag	atg	96
Phe	Arg	His	Gly	Ser	Leu	Ile	Ser	Ile	Asp	Ser	Thr	Cys	Thr	Glu	Met	
			20					25					30			
ggc	aat	ttt	gac	aat	gct	aat	gtc	act	gga	gaa	ata	gaa	ttt	gcc	att	144
Gly	Asn	Phe	Asp	Asn	Ala	Asn	Val	Thr	Gly	Glu	Ile	Glu	Phe	Ala	Ile	
		35					40					45				
cat	tat	tgc	ttc	aaa	acc	cat	tct	tta	gaa	ata	tgc	atc	aag	gcc	tgt	192
His	Tyr	Cys	Phe	Lys	Thr	His	Ser	Leu	Glu	Ile	Cys	Ile	Lys	Ala	Cys	
	50					55					60					
aag	aac	ctt	gcc	tat	gga	gaa	gaa	aag	aag	aaa	aag	tgc	aat	ccg	tat	240
Lys	Asn	Leu	Ala	Tyr	Gly	Glu	Glu	Lys	Lys	Lys	Lys	Cys	Asn	Pro	Tyr	
65					70					75					80	
gtg	aag	acc	tac	ctg	ttg	ccc	gac	aga	tcc	tcc	cag	gga	aag	cgc	aag	288
Val	Lys	Thr	Tyr	Leu	Leu	Pro	Asp	Arg	Ser	Ser	Gln	Gly	Lys	Arg	Lys	
				85					90					95		
act	gga	gtc	caa	agg	aac	acc	gtg	gac	ccg	acc	ttt	cag	gag	acc	ttg	336
Thr	Gly	Val	Gln	Arg	Asn	Thr	Val	Asp	Pro	Thr	Phe	Gln	Glu	Thr	Leu	
			100					105					110			
aag	tat	cag	gtg	gcc	cct	gcc	cag	ctg	gtg	acc	cgg	cag	ctg	cag	gtc	384
Lys	Tyr	Gln	Val	Ala	Pro	Ala	Gln	Leu	Val	Thr	Arg	Gln	Leu	Gln	Val	
		115					120					125				
tcg	gtg	tgg	cat	ctg	ggc	acg	ctg	gcc	cgg	aga	gtg	ttt	ctt	gga	gaa	432
Ser	Val	Trp	His	Leu	Gly	Thr	Leu	Ala	Arg	Arg	Val	Phe	Leu	Gly	Glu	
	130					135					140					

st0005seq

```

gtg atc att tct ctg gcc acg tgg gac ttt gaa gac agc aca aca cag 480
Val Ile Ile Ser Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln
145 150 155 160

tcc ttc cgc tgg cat ccg ctc cgg gcc aag gcg gag aaa tac gaa gac 528
Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp
165 170 175

agc gtt cct cag agt aat gga gag ctc aca gtc cgg gct aag ctg gtt 576
Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu Val
180 185 190

ctc cct tca cgg ccc aga aaa ctc caa gag gct caa gaa ggg aca gat 624
Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp
195 200 205

cag cca tca ctt cat ggt caa ctt tgt ttg gta gtg cta gga gcc aag 672
Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala Lys
210 215 220

aat tta cct gtg cgg cca gat ggc acc ttg aac tca ttt gtt aag ggc 720
Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys Gly
225 230 235 240

tgt ctc act ctg cca gac caa caa aaa ctg aga ctg aag tcg cca gtc 768
Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro Val
245 250 255

ctg agg aag cag gct tgc ccc cag tgg aaa cac tca ttt gtc ttc agt 816
Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe Ser
260 265 270

ggc gta acc cca gct cag ctg agg cag tcg agc ttg gag tta act gtc 864
Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr Val
275 280 285

tgg gat cag gcc ctc ttt gga atg aat gac cgc ttg ctt gga gga acc 912
Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly Thr
290 295 300

aga ctt ggt tca aag gga gac aca gct gtt ggc ggg gat gca tgc tca 960
Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys Ser
305 310 315 320

cta tcg aag ctc cag tgg cag aaa gtc ctt tcc agc ccc aat cta tgg 1008
Leu Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu Trp
325 330 335

aca gac atg act ctt gtc ctg cac tgacatgaag gcctcaaggt tccaggttgc 1062
Thr Asp Met Thr Leu Val Leu His

agcagggcgtg aggcactgtg cgtctgcaga ggggctacga accaggtgca ggggtcccagc 1122

tggagacccc tttgaccttg agcagtctcc atctgcggcc ctgtcccatg gcttaaccgc 1182

ctattggtat ctgtgtatat ttacgttaaa cacaattatg ttacctaagc ctctggtggg 1242

ttatctcctc tttgagatgt agaaaatggc cagatttttaa taaacgttgt tacccatgaa 1302
aaaaaaaaa a 1313

```

st0005seq

<210> 2
 <211> 344
 <212> PRT
 <213> Homo sapiens

<400> 2
 Gln Asn Leu Pro Ser Ser Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly
 1 5 10 15
 Phe Arg His Gly Ser Leu Ile Ser Ile Asp Ser Thr Cys Thr Glu Met
 20 25 30
 Gly Asn Phe Asp Asn Ala Asn Val Thr Gly Glu Ile Glu Phe Ala Ile
 35 40 45
 His Tyr Cys Phe Lys Thr His Ser Leu Glu Ile Cys Ile Lys Ala Cys
 50 55 60
 Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr
 65 70 75 80
 Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys
 85 90 95
 Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr Leu
 100 105 110
 Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln Val
 115 120 125
 Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly Glu
 130 135 140
 Val Ile Ile Ser Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln
 145 150 155 160
 Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp
 165 170 175
 Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu Val
 180 185 190
 Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp
 195 200 205
 Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala Lys
 210 215 220
 Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys Gly
 225 230 235 240
 Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro Val
 245 250 255
 Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe Ser
 260 265 270
 Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr Val
 275 280 285
 Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly Thr
 290 295 300

st0005seq

Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys Ser
305 310 315 320

Leu Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu Trp
325 330 335

Thr Asp Met Thr Leu Val Leu His
340

<210> 3

<211> 471

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(471)

<400> 3

gga agt cca gca ggt aga tca atc tac aac agc ttt tat gtg tat tgc 48
Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn Ser Phe Tyr Val Tyr Cys
1 5 10 15

aaa ggc ccc tgt caa aga gtg cag ccg gga aaa ctc agg gta cag tgc 96
Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln Cys
20 25 30

agc acc tgc agg cag gca acg ctc acc ttg acc cag ggt cca tct tgc 144
Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu Thr Gln Gly Pro Ser Cys
35 40 45

tgg gat gat gtt tta att cca aac cgg atg agt ggt gaa tgc caa tcc 192
Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser
50 55 60

cca cac tgc cct ggg act agt gca gaa ttt ttc ttt aaa tgt gga gca 240
Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly Ala
65 70 75 80

cac ccc acc tct gac aag gaa aca tca gta gct ttg cac ctg atc gca 288
His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile Ala
85 90 95

aca aat agt cgg aac atc act tgc att acg tgc aca gac gtc agg agc 336
Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg Ser
100 105 110

ccc gtc ctg gtt ttc cag tgc aac tcc cgc cac gtg att tgc tta gac 384
Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu Asp
115 120 125

tgt ttc cac tta tac tgt gtg aca aga ctc aat gat cgg cag ttt gtt 432
Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val
130 135 140

cac gac cct caa ctt ggc tac tcc ctg cct tgt gtg tag 471
His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val
145 150 155

<210> 4

st0005seq

<211> 156
<212> PRT
<213> Homo sapiens

<400> 4

```

Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn Ser Phe Tyr Val Tyr Cys
 1      5      10      15
Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln Cys
 20      25      30
Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu Thr Gln Gly Pro Ser Cys
 35      40      45
Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser
 50      55      60
Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly Ala
 65      70      75      80
His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile Ala
 85      90      95
Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg Ser
100      105      110
Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu Asp
115      120      125
Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val
130      135      140
His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val
145      150      155

```

<210> 5
<211> 27
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence:Oligonucleotide

<400> 5

ttaagaattc ggaagtccag caggtag

27

<210> 6
<211> 29
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence:Oligonucleotide

<400> 6

attaggatcc ctacacacaa ggcagggag

29

<210> 7
<211> 19
<212> DNA
<213> Artificial sequence

<220>

<223> Description of the artificial sequence:Oligonucleotide

<400> 7

gcgtttggaa tcactacag

19

st0005seq

<210> 8
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:Oligonucleotide

<400> 8
ggtctcgggtg tggcatc 17

<210> 9
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:Oligonucleotide

<400> 9
ccgcttgctt ggaggaac 18

<210> 10
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:Oligonucleotide

<400> 10
cgtatttctc cgccttgg 18

<210> 11
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:Oligonucleotide

<400> 11
aatagctcga gtcagtgcag gacaagag 28

<210> 12
<211> 2347
<212> DNA
<213> Homo sapiens

<400> 12
ggccttgagg cactgagga tgccagttct gcctgttcat ctggaacctg gatctaagga 60
gggaagaggc gttgcccctg ctggcatagt caggtaccag cccagccagg tattgaacgg 120
gctgagcttt tcatgatggt tcctgctgac ctggaaacat cttaaattgga agggcgtgag 180
cgcttggtcc atgcagtga gctcttccaa cctgggtcaa cgaaaacgga gaagaaatgg 240
cccaagaaat agatctgagt gctctcaagg agttagaacg cgaggccatt ctccaggtcc 300
tgtaccgaga ccaggcgggt caaaacacag aggaggagag gacacggaaa ctgaaaacac 360
acctgcagca tctccggtgg aaaggagcga agaacacgga ctgggagcac aaagagaagt 420
gtgtgctgcg ctgccagcag gtgctggggg tcctgctgca ccggggcgcc gtgtgccggg 480

st0005seq

```

gctgcagcca cgcggtgtgt gcccagtgcc gagtgttcct gaggggggacc catgcctgga 540
agtgcacggt gtgcttcgag gacaggaatg tcaaaataaa aactggagaa tggttctatg 600
aggaacgagc caagaaattt ccaactggag gcaaactatga gacagttgga gggcagctct 660
tgcaatctta tcagaagctg agcaaaattt ctgtggttcc tcctactcca cctcctgtca 720
gcgagagcca gtgcagccgc agtcctggca ggttacagga atttggtcag tttagaggat 780
ttaataagtc cgtggaaaat ttgtttctgt ctcttgctac ccacgtgaaa aagctctcca 840
aatcccagaa tgatatgact tctgagaagc atcttctcgc cacggggccc aggcagtggt 900
tgggacagac agagagacgg agccagtcgt acactgcggt caacgtcacc accaggaagg 960
tcagtgcacc agatattctg aaacctctca atcaagagga tcccaaatgc tctactaacc 1020
ctattttgaa gcaacagaat ctcccatcca gtccggcacc cagtaccata ttctctggag 1080
gttttagaca cggaagttaa attagcattg acagcacctg tacagagatg ggcaattttg 1140
acaatgctaa tgtcactgga gaaatagaat ttgccattca ttattgcttc aaaaccatt 1200
ctttagaaat atgcatcaag gcctgtaaga acctgccta tggagaagaa aagaagaaaa 1260
agtgcaatcc gtatgtgaag acctacctgt tgcccagacag atcctcccag ggaaagcgca 1320
agactggagt ccaaaggaac accgtggacc cgacctttca ggagacctg aagtatcagg 1380
tggccctgtc ccagctggtg acccggcagc tgcaggtctc ggtgtggcat ctgggcacgc 1440
tggcccgag agtggtttct ggagaagtga tcattcctct ggccacgtgg gactttgaag 1500
acagcacaac acagtccttc cgctggcatc cgctccgggc caaggcgag aaatacgaag 1560
acagcgttcc tcagagtaat ggagagctca cagtccgggc taagctgggt ctcccttcac 1620
ggcccagaaa actccaagag gctcaagaag ggacagatca gccatcactt catggtcaac 1680
tttgtttggt agtgctagga gccaaagaat tacctgtgcg gccagatggc accttgaact 1740
catttggttaa gggctgtctc actctgccag accaacaata actgagactg aagtcgccag 1800
tcctgaggaa gcaggcttgc ccccagtgga aacactcatt tgtcttcagt ggcgtaacct 1860
cagctcagct gaggcagtcg agcttggagt taactgtctg ggatcaggcc ctctttggaa 1920
tgaacgaccg cttgcttgga ggaaccagac ttggttcaaa gggagacaca gctgttggcg 1980
gggatgcatg ctcacaatcg aagctccagt ggagaaaagt cctttccagc cccaatctat 2040
ggacagacat gactcttgtc ctgcactgac atgaaggcct caaggttcca ggttgacgca 2100
ggcgtgaggg actgtgcgtc tgcagagggg ctacgaacca ggtgcagggt cccagctgga 2160
gacccctttg accttgagca gtctccatct gcggccctgt cccatggctt aaccgcctat 2220
tggtatctgt gtatatattac gttaaacaca attatgttac ctaagcctct ggtgggttat 2280
ctcctctttg agatgtagaa aatggccaga ttttaataaa cgttgttacc catgaaaaaa 2340
aaaaaaa
2347

```

<210> 13
 <211> 610
 <212> PRT
 <213> Homo sapiens

<400> 13

```

Met Ala Gln Glu Ile Asp Leu Ser Ala Leu Lys Glu Leu Glu Arg Glu
1          5          10          15
Ala Ile Leu Gln Val Leu Tyr Arg Asp Gln Ala Val Gln Asn Thr Glu
20          25          30
Glu Glu Arg Thr Arg Lys Leu Lys Thr His Leu Gln His Leu Arg Trp
35          40          45
Lys Gly Ala Lys Asn Thr Asp Trp Glu His Lys Glu Lys Cys Cys Ala
50          55          60
Arg Cys Gln Gln Val Leu Gly Phe Leu Leu His Arg Gly Ala Val Cys
65          70          75          80
Arg Gly Cys Ser His Arg Val Cys Ala Gln Cys Arg Val Phe Leu Arg
85          90          95
Gly Thr His Ala Trp Lys Cys Thr Val Cys Phe Glu Asp Arg Asn Val
100         105         110
Lys Ile Lys Thr Gly Glu Trp Phe Tyr Glu Glu Arg Ala Lys Lys Phe
115         120         125

```

st0005seq

Pro Thr Gly Gly Lys His Glu Thr Val Gly Gly Gln Leu Leu Gln Ser
130 135 140

Tyr Gln Lys Leu Ser Lys Ile Ser Val Val Pro Pro Thr Pro Pro Pro
145 150 155 160

Val Ser Glu Ser Gln Cys Ser Arg Ser Pro Gly Arg Leu Gln Glu Phe
165 170 175

Gly Gln Phe Arg Gly Phe Asn Lys Ser Val Glu Asn Leu Phe Leu Ser
180 185 190

Leu Ala Thr His Val Lys Lys Leu Ser Lys Ser Gln Asn Asp Met Thr
195 200 205

Ser Glu Lys His Leu Leu Ala Thr Gly Pro Arg Gln Cys Val Gly Gln
210 215 220

Thr Glu Arg Arg Ser Gln Ser Asp Thr Ala Val Asn Val Thr Thr Arg
225 230 235 240

Lys Val Ser Ala Pro Asp Ile Leu Lys Pro Leu Asn Gln Glu Asp Pro
245 250 255

Lys Cys Ser Thr Asn Pro Ile Leu Lys Gln Gln Asn Leu Pro Ser Ser
260 265 270

Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly Phe Arg His Gly Ser Leu
275 280 285

Ile Ser Ile Asp Ser Thr Cys Thr Glu Met Gly Asn Phe Asp Asn Ala
290 295 300

Asn Val Thr Gly Glu Ile Glu Phe Ala Ile His Tyr Cys Phe Lys Thr
305 310 315 320

His Ser Leu Glu Ile Cys Ile Lys Ala Cys Lys Asn Leu Ala Tyr Gly
325 330 335

Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr Val Lys Thr Tyr Leu Leu
340 345 350

Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys Thr Gly Val Gln Arg Asn
355 360 365

Thr Val Asp Pro Thr Phe Gln Glu Thr Leu Lys Tyr Gln Val Ala Pro
370 375 380

Ala Gln Leu Val Thr Arg Gln Leu Gln Val Ser Val Trp His Leu Gly
385 390 395 400

Thr Leu Ala Arg Arg Val Phe Leu Gly Glu Val Ile Ile Pro Leu Ala
405 410 415

Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln Ser Phe Arg Trp His Pro
420 425 430

Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp Ser Val Pro Gln Ser Asn
435 440 445

Gly Glu Leu Thr Val Arg Ala Lys Leu Val Leu Pro Ser Arg Pro Arg
450 455 460

st0005seq

Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp Gln Pro Ser Leu His Gly
 465 470 475 480
 Gln Leu Cys Leu Val Val Leu Gly Ala Lys Asn Leu Pro Val Arg Pro
 485 490 495
 Asp Gly Thr Leu Asn Ser Phe Val Lys Gly Cys Leu Thr Leu Pro Asp
 500 505 510
 Gln Gln Lys Leu Arg Leu Lys Ser Pro Val Leu Arg Lys Gln Ala Cys
 515 520 525
 Pro Gln Trp Lys His Ser Phe Val Phe Ser Gly Val Thr Pro Ala Gln
 530 535 540
 Leu Arg Gln Ser Ser Leu Glu Leu Thr Val Trp Asp Gln Ala Leu Phe
 545 550 555 560
 Gly Met Asn Asp Arg Leu Leu Gly Gly Thr Arg Leu Gly Ser Lys Gly
 565 570 575
 Asp Thr Ala Val Gly Gly Asp Ala Cys Ser Gln Ser Lys Leu Gln Trp
 580 585 590
 Gln Lys Val Leu Ser Ser Pro Asn Leu Trp Thr Asp Met Thr Leu Val
 595 600 605
 Leu His
 610

<210> 14

<211> 1648

<212> DNA

<213> Homo sapiens

<400> 14

gaaatcatgc	ccctcgtaga	gcagcaggtc	caagcagggc	tgctggctat	ttttccaaaa	60
agtgaggcag	tttaaaaaaa	agggcgagaa	ctagaattat	agaataatgg	cacattttgt	120
gtattttgtaa	aactaacggc	ttgcatgggt	cacaacccat	ttcttatgcc	tgtgttttcc	180
ttggcagcaa	aatttctgtg	gttcctccta	ctccacctcc	tgtcagcgag	agccagtgc	240
gccgcagtcc	tggcaggaag	gtcagtgcac	cagatattct	gaaacctctc	aatcaagagg	300
atcccaaagt	cttactaac	cctattttga	agcaacagaa	tctcccatcc	agtcgggcac	360
ccagtaccat	atttctctgga	ggtttttagac	acggaagttt	aattagcatt	gacagcacct	420
gtacagagat	gggcaatttt	gacaatgcta	atgtcactgg	agaaatagaa	tttgccattc	480
attattgctt	caaaaacccat	tcttttagaaa	tatgcatcaa	ggcctgtaag	aaccttgcc	540
atggagaaga	aaagaagaaa	aagtgcattc	cgtatgtgaa	gacctacctg	ttgcccagca	600
gatcctccca	gggaaagcgc	aagactggag	tccaaaggaa	caccgtggac	ccgacctttc	660
aggagacctt	gaagtatcag	gtggccccctg	cccagctggg	gacccggcag	ctgcaggctt	720
cggtgtggca	tctgggcacg	ctggccccgga	gagtgtttct	tggagaagtg	atcatttcct	780
tggccacgtg	ggactttgaa	gacagcacaa	cacagtcctt	ccgctggcat	ccgctccggg	840
ccaaggcgga	gaaatacgaa	gacagcggtc	ctcagagtaa	tggagagctc	acagtccggg	900
ctaagctggt	tctcccttca	cggccccagaa	aactccaaga	ggctcaagaa	gggacagatc	960
agccatcact	tcatgggtcaa	ctttgtttgg	tagtgctagg	agccaagaat	ttacctgtgc	1020
ggccagatgg	caccttgaac	tcatttggtta	agggctgtct	cactctgcca	gaccaacaaa	1080
aactgagact	gaagtcgcca	gtcctgagga	agcaggcttg	ccccagtg	aaacactcat	1140
ttgtcttcag	tggcgtaacc	cgagctcagc	tgaggcagtc	gagcttgag	ttactgtct	1200
gggatcaggc	cctctttgga	atgaacgacc	gcttgcttgg	aggaaccaga	cttggttcaa	1260
aggagacac	agctgttgcc	ggggatgcat	gtcaccaatc	gaagctccag	tggcagaaag	1320
tccittccag	ccccaatcta	tggacagaca	tgactcttgt	cctgcactga	catgaaggcc	1380
tcaaggttcc	aggttgcagc	aggcgtgagg	cactgtgcgt	ctgcagaggg	gctacgaacc	1440
aggtgcaggg	tcccagctgg	agaccccttt	gaccttgagc	agtctccatc	tgcgccctg	1500

st0005seq

tcccatggct taaccgccta ttggtatctg tgtatatatta cgttaaacac aattatgtta 1560
cctaagcctc tgggtgggtta tctcctcttt gagatgtaga aaatggccag attttaataa 1620
acgttggttac ccatgaaaaa aaaaaaaa 1648

<210> 15
<211> 313
<212> PRT
<213> Homo sapiens

<400> 15
Met Gly Asn Phe Asp Asn Ala Asn Val Thr Gly Glu Ile Glu Phe Ala
1 5 10 15
Ile His Tyr Cys Phe Lys Thr His Ser Leu Glu Ile Cys Ile Lys Ala
20 25 30
Cys Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Cys Asn Pro
35 40 45
Tyr Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg
50 55 60
Lys Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr
65 70 75 80
Leu Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln
85 90 95
Val Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly
100 105 110
Glu Val Ile Ile Pro Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr
115 120 125
Gln Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu
130 135 140
Asp Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu
145 150 155 160
Val Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr
165 170 175
Asp Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala
180 185 190
Lys Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys
195 200 205
Gly Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro
210 215 220
Val Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe
225 230 235 240
Ser Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr
245 250 255
Val Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly
260 265 270
Thr Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys
Page 10

st0005seq

275 280 285
 Ser Gln Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu
 290 295 300
 Trp Thr Asp Met Thr Leu Val Leu His
 305 310

<210> 16
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 16
 ccagttctgc ctgttcac 19

<210> 17
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 17
 ttcaaaacac agaggaggag 20

<210> 18
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 18
 gaatttggtc agttagagg 20

<210> 19
 <211> 26
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 19
 ttctgggatt tggagagctt tttcac 26

<210> 20
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>

st0005seq

<223> Description of the artificial sequence:oligonucleotide

<400> 20
tctgtctgtc ccacacactg cc 22

<210> 21
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 21
gactggctcc gtctctctg 19

<210> 22
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 22
aagcaacaga atctcccatc c 21

<210> 23
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 23
gcattgtcaa aattgcccac c 21

<210> 24
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 24
aggcggagaa atacgaagac 20

<210> 25
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:oligonucleotide

<400> 25

gcagagtgag acagccctta ac

22

<210> 26

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:oligonucleotide

<400> 26

cttcctcagg actggcgact tcag

24

<210> 27

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:oligonucleotide

<400> 27

caagcggtcg ttcattccaa agag

24

<210> 28

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:oligonucleotide

<400> 28

aagaggagat aaccaccag ag

22

<210> 29

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:oligonucleotide

<400> 29

agggctgctg gctatttttc

20

<210> 30

<211> 19

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:oligonucleotide

<400> 30

taagaaatgg gttgtgaac

19

st0005seq

<210> 31
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 31
 aagcaacaga atctcccatc c 21

<210> 32
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 32
 gcattgtcaa aattgcccac c 21

<210> 33
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 33
 aggcggagaa atacgaagac 20

<210> 34
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 34
 gcagagtga acagccctta ac 22

<210> 35
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence:oligonucleotide

<400> 35
 cttcctcagg actggcgact tcag 24

<210> 36
 <211> 24
 <212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:oligonucleotide

<400> 36

caagcggtcg ttcattccaa agag

24

<210> 37

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:oligonucleotide

<400> 37

aagaggagat aacccaccag ag

22

<210> 38

<211> 18

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:oligonucleotide

<400> 38

aatggaaggg cgtgacgc

18

<210> 39

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:oligonucleotide

<400> 39

cctcacgcct gctgcaacct g

21

<210> 40

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:oligonucleotide

<400> 40

gcacgaattc atggcccaag aaatagatct g

31

<210> 41

<211> 24

<212> DNA

<213> Artificial sequence

<220>

st0005seq

<223> Description of the artificial sequence:oligonucleotide

<400> 41

ctgtcttcgt atttctccgc cttg

24

<210> 42

<211> 2347

<212> DNA

<213> Homo sapiens

<400> 42

ggccttgggg cactgagggg tgccagttct gcctgttcat ctggaacctg gatctaagga 60
gggaagaggc gttgcccctg ctggcatagt caggtaggag cccagccagg tattgaacgg 120
gctgagcttt tcatgatggt tcctgctgac ctggaacat cttaaaggga agggcgtgag 180
cgcttggtcc atgcagtgaa gctcttccaa cctgggtcaa cgaaaacgga gaagaaatgg 240
cccaagaaat agatctgagt gctctcaagg agttagaacg cgaggccatt ctccagggtcc 300
tgtaccgaga ccaggcggtt caaaacacag aggaggagag gacacggaaa ctgaaaaacac 360
acctgcagca tctccggttg aaaggagcga agaacacgga ctgggagcac aaagagaagt 420
gctgtgcgcg ctgccagcag gtgctggggt tcctgctgca ccggggcgcc gtgtgccggg 480
gctgcagcca ccgcgtgtgt gccagtgcc gagtgttcct gagggggacc catgcctgga 540
agtgcacggt gtgcttcgag gacaggaatg tcaaaataaa aactggagaa tggttctatg 600
aggaaacgag caagaaatct ccaactggag gcaaacatga gacagttgga gggcagctct 660
tgcaatctta tcagaagctg agcaaaatct ctgtggttcc tcctactcca cctcctgtca 720
gcgagagcca gtgcagccgc agtcctggca gggtacagga atttggtcag tttagaggat 780
ttaataagtc cgtggaaaaa ttgtttctgt ctcttgctac ccacgtgaaa aagctctcca 840
aatcccagaa tgatatgact tctgagaagc atcttctcgc cacgggcccc aggcagtggtg 900
tgggacagac agagagacgg agccagtcgt acaactgcgg caacgtcacc accaggaagg 960
tcagtgcacc agatattctg aaacctctca atcaagagga tcccaaatgc tctactaacc 1020
ctattttgaa gcaacagaat ctcccatcca gtccggcacc cagtaccata ttctctggag 1080
gttttagaca cggaagttta attagcattg acagcacctg tacagagatg ggcaattttg 1140
acaatgctaa tgtcactgga gaaatagaat ttgccattca ttattgcttc aaaacccatt 1200
ctttagaaat atgcatcaag gcctgtaaga acctgacctg tggagaagaa aagaagaaaa 1260
agtgcaatcc gtatgtgaag acctacctgt tgcccagacag atcctcccag ggaaagcgca 1320
agactggagt ccaaaggaac accgtggacc cgacctttca ggagacctg aagtatcagg 1380
tggccctcgc ccagctgggtg acccggcagc gtcaggtctc ggtgtggcat ctgggcacgc 1440
tggcccgag agtgtttctt ggagaagtga tcattcctct ggccacgtgg gactttgaag 1500
acagcacaac acagtccttc cgctggcatc cgctccgggc caaggcggag aaatacgaag 1560
acagcgttcc tcagagtaat ggagagctca cagtccgggc taagctgggt ctcccttcac 1620
ggcccagaaa actccaagag gctcaagaag ggacagatca gccatcactt catggtcaac 1680
tttgtttgg agtgctagga agtctgaccg accaagaaat tacctgtgcg gccagatggc acctgaact 1740
catttggtta gggctgtctc actctgccag accaacaaaa actgagactg aagtcgccag 1800
tcctgaggaa gcaggcttgc cccagtgga aacactcatt tgtcttcagt ggcgttaacc 1860
cagctcagct gaggcagtcg agcttgaggt taactgtctg ggatcaggcc ctctttggaa 1920
tgaacgaccg ctgtcttgga ggaaccagac ttggttcaaa gggagacaca gctgttggcg 1980
gggatgcatg ctcaaatcg aagctccagt ggcagaaagt ctttccagc cccaatctat 2040
ggacagacat gactcttgtc ctgcactgac atgaaggcct caaggttcca ggttgacgca 2100
ggcgtgaggc actgtgcgtc tgcagagggg ctacgaacca ggtgcagggt cccagctgga 2160
gacccctttg accttgagca gtctccatct gcggccctgt cccatggctt aaccgcctat 2220
tggatatctgt gtatatattac gttaaacaca attatgttac ctaagcctct ggtgggttat 2280
ctcctctttg agatgtagaa aatggccaga ttttaataaa cgttgttacc catgaaaaaa 2340
aaaaaaa 2347

<210> 43

<211> 610

<212> PRT

<213> Homo sapiens

<400> 43

Met Ala Gln Glu Ile Asp Leu Ser Ala Leu Lys Glu Leu Glu Arg Glu
1 5 10 15

st0005seq

Ala Ile Leu Gln Val Leu Tyr Arg Asp Gln Ala Val Gln Asn Thr Glu
 20 25 30
 Glu Glu Arg Thr Arg Lys Leu Lys Thr His Leu Gln His Leu Arg Trp
 35 40 45
 Lys Gly Ala Lys Asn Thr Asp Trp Glu His Lys Glu Lys Cys Cys Ala
 50 55 60
 Arg Cys Gln Gln Val Leu Gly Phe Leu Leu His Arg Gly Ala Val Cys
 65 70 75 80
 Arg Gly Cys Ser His Arg Val Cys Ala Gln Cys Arg Val Phe Leu Arg
 85 90 95
 Gly Thr His Ala Trp Lys Cys Thr Val Cys Phe Glu Asp Arg Asn Val
 100 105 110
 Lys Ile Lys Thr Gly Glu Trp Phe Tyr Glu Glu Arg Ala Lys Lys Phe
 115 120 125
 Pro Thr Gly Gly Lys His Glu Thr Val Gly Gly Gln Leu Leu Gln Ser
 130 135 140
 Tyr Gln Lys Leu Ser Lys Ile Ser Val Val Pro Pro Thr Pro Pro Pro
 145 150 155 160
 Val Ser Glu Ser Gln Cys Ser Arg Ser Pro Gly Arg Leu Gln Glu Phe
 165 170 175
 Gly Gln Phe Arg Gly Phe Asn Lys Ser Val Glu Asn Leu Phe Leu Ser
 180 185 190
 Leu Ala Thr His Val Lys Lys Leu Ser Lys Ser Gln Asn Asp Met Thr
 195 200 205
 Ser Glu Lys His Leu Leu Ala Thr Gly Pro Arg Gln Cys Val Gly Gln
 210 215 220
 Thr Glu Arg Arg Ser Gln Ser Asp Thr Ala Val Asn Val Thr Thr Arg
 225 230 235 240
 Lys Val Ser Ala Pro Asp Ile Leu Lys Pro Leu Asn Gln Glu Asp Pro
 245 250 255
 Lys Cys Ser Thr Asn Pro Ile Leu Lys Gln Gln Asn Leu Pro Ser Ser
 260 265 270
 Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly Phe Arg His Gly Ser Leu
 275 280 285
 Ile Ser Ile Asp Ser Thr Cys Thr Glu Met Gly Asn Phe Asp Asn Ala
 290 295 300
 Asn Val Thr Gly Glu Ile Glu Phe Ala Ile His Tyr Cys Phe Lys Thr
 305 310 315 320
 His Ser Leu Glu Ile Cys Ile Lys Ala Cys Lys Asn Leu Ala Tyr Gly
 325 330 335
 Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr Val Lys Thr Tyr Leu Leu
 340 345 350

st0005seq

Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys Thr Gly Val Gln Arg Asn
 355 360 365
 Thr Val Asp Pro Thr Phe Gln Glu Thr Leu Lys Tyr Gln Val Ala Pro
 370 375 380
 Ala Gln Leu Val Thr Arg Gln Leu Gln Val Ser Val Trp His Leu Gly
 385 390 395 400
 Thr Leu Ala Arg Arg Val Phe Leu Gly Glu Val Ile Ile Pro Leu Ala
 405 410 415
 Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln Ser Phe Arg Trp His Pro
 420 425 430
 Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp Ser Val Pro Gln Ser Asn
 435 440 445
 Gly Glu Leu Thr Val Arg Ala Lys Leu Val Leu Pro Ser Arg Pro Arg
 450 455 460
 Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp Gln Pro Ser Leu His Gly
 465 470 475 480
 Gln Leu Cys Leu Val Val Leu Gly Ala Lys Asn Leu Pro Val Arg Pro
 485 490 495
 Asp Gly Thr Leu Asn Ser Phe Val Lys Gly Cys Leu Thr Leu Pro Asp
 500 505 510
 Gln Gln Lys Leu Arg Leu Lys Ser Pro Val Leu Arg Lys Gln Ala Cys
 515 520 525
 Pro Gln Trp Lys His Ser Phe Val Phe Ser Gly Val Thr Pro Ala Gln
 530 535 540
 Leu Arg Gln Ser Ser Leu Glu Leu Thr Val Trp Asp Gln Ala Leu Phe
 545 550 555 560
 Gly Met Asn Asp Arg Leu Leu Gly Gly Thr Arg Leu Gly Ser Lys Gly
 565 570 575
 Asp Thr Ala Val Gly Gly Asp Ala Cys Ser Gln Ser Lys Leu Gln Trp
 580 585 590
 Gln Lys Val Leu Ser Ser Pro Asn Leu Trp Thr Asp Met Thr Leu Val
 595 600 605
 Leu His
 610

<210> 44
 <211> 1648
 <212> DNA
 <213> Homo sapiens

<400> 44
 gaaatcatgc ccctcgtaga gcagcaggtc caagcagggc tgctggctat ttttcaaaa 60
 agtgaggcag ttttaaaaaa aggcggagaa ctagaattat agaataatgg cacattttgt 120
 gtatttgtaa aactaacggc ttgcatgggt cacaacccat ttcttatgcc tgtgttttcc 180
 ttggcagcaa aatttctgtg gttcctccta ctccacctcc tgtcagcgag agccagtgca 240
 gccgcagtc tggcaggaag gtcagtgcac cagatattct gaaacctctc aatcaagagg 300

st0005seq

```

atcccaaagt ctctactaac cctattttga agcaacagaa tctcccatcc agtccggcac 360
ccagtagcat attctctgga ggttttagac acggaagttt aattagcatt gacagcacct 420
gtacagagat gggcaatttt gacaatgcta atgtcactgg agaaatagaa tttgccattc 480
attattgctt caaaacccat tctttagaaa tatgcatcaa ggcctgtaag aaccttgctt 540
atggagaaga aaagaagaaa aagtgcatac cgtatgtgaa gacctacctg ttgcccagaa 600
gatcctccca gggaaagcgc aagactggag tccaaaggaa caccgtggac ccgacctttc 660
aggagacctt gaagtatcag gtggcccctg cccagctggt gacccggcag ctgcaggtct 720
cgggtgtggc tctgggcacg ctggcccggg gagggtttct tggagaagtg atcattcctc 780
tggccacgtg ggactttgaa gacagcacia cacagtcctt ccgctggcat ccgctccggg 840
ccaaggcgga gaaatacgaa gacagcgttc ctcagagtaa tggagagctc acagtccggg 900
ctaagctggt tctcccttca cggcccagaa aactccaaga ggctcaagaa gggacagatc 960
agccatcact tcatggtcaa ctttgtttgg tagtgctagg agccaagaat ttacctgtgc 1020
ggccagatgg caccittgaa tcatttgtaa agggctgtct cactctgcca gaccaacaaa 1080
aactgagact gaagtgcgca gtcttgagga agcaggcttg cccccagtgg aaacactcat 1140
ttgtcttcag tggcgtaacc ccagctcagc tgaggcagtc gagcttggag ttaactgtct 1200
gggatcaggc cctcttttga atgaacgacc gcttgcttgg aggaaccaga cttggttcaa 1260
agggagacac agctgttggc ggggatgcac gctcacaatc gaagctccag tggcagaaag 1320
tcctttccag ccccaatcta tggacagaca tgactcttgt cctgcactga catgaaggcc 1380
tcaaggttcc aggttgcagc aggcgtgagg cactgtgcgt ctgcagaggg gctacgaacc 1440
aggtgcaggg tcccagctgg agaccccttt gaccttgagc agtctccatc tgcggccctg 1500
tcccattggt taaccgccta ttggtatctg tgtatattta cgtaaacac aattatgtta 1560
cctaagcctc tgggtgggta tctcctcttt gagatgtaga aaatggccag attttaataa 1620
acgttggtac ccatgaaaaa aaaaaaaaaa

```

<210> 45
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 45
 Met Gly Asn Phe Asp Asn Ala Asn Val Thr Gly Glu Ile Glu Phe Ala
 1 5 10 15
 Ile His Tyr Cys Phe Lys Thr His Ser Leu Glu Ile Cys Ile Lys Ala
 20 25 30
 Cys Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Lys Cys Asn Pro
 35 40 45
 Tyr Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg
 50 55 60
 Lys Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr
 65 70 75 80
 Leu Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln
 85 90 95
 Val Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly
 100 105 110
 Glu Val Ile Ile Pro Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr
 115 120 125
 Gln Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu
 130 135 140
 Asp Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu
 145 150 155 160
 Val Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr
 165 170 175

st0005seq

Asp Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala
180 185 190
Lys Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys
195 200 205
Gly Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro
210 215 220
Val Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe
225 230 235 240
Ser Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr
245 250 255
Val Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly
260 265 270
Thr Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys
275 280 285
Ser Gln Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu
290 295 300
Trp Thr Asp Met Thr Leu Val Leu His
305 310

<210> 46

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:oligonucleotide

<400> 46

tcgtagagca gcaggtccaa g

21